AMENDMENTS TO THE CLAIMS:

This listing of claims will replace all prior versions, and listings, of claims in the application:

LISTING OF CLAIMS:

Claims 1-17 (canceled)

Claim 18. (Previously Presented) A method for topographic genotyping comprising the steps of:

placing a biological specimen having DNA of a patient under a microscope;

inspecting the biological specimen microscopically with the microscope;

choosing a microscopic sized target on the biological specimen based on its histopathologic characteristics;

separating the target from the specimen;

extracting DNA from the target in an aqueous solution, wherein the extraction does not include DNA precipitation;

centrifuging the aqueous solution from the extraction step directly from the DNA extracting step to create a pellet and a DNA-containing supernatant;

removing the DNA-containing supernatant so that the DNA sequences therein can be amplified;

amplifying the DNA sequences of the DNA-containing supernatant; and

detecting mutations in the DNA sequences.

Claim 19. (Previously Presented) A method according to Claim 18, wherein the biological specimen is fixative treated tissue.

Claim 20. (Previously Presented) A method according to Claim 18, wherein the biological specimen is a tissue section, cytological fluid, filter or cellular specimen.

Claim 21. (Previously Presented) A method according to Claim 18, wherein the specimen is a tissue section, and the separating step further includes slicing the target from the tissue section and placing the target on a glass slide.

Claim 22. (Previously Presented) A method according to Claim 18, wherein the specimen is a tissue section, and the separating step further placing the target in a tube.

Claim 23. (Previously Presented) A method according to Claim 18, wherein the separating step further includes cutting an arc segment from the specimen, and placing the segment in a tube.

Claim 24. (Previously Presented) A method according to Claim 18, wherein the extracting step further includes placing the target in a lysis buffer.

Claim 25. (Previously Presented) A method according to Claim 24, wherein the extracting step further includes contacting the target with proteinase K.

Claim 26. (Previously Presented) A method according to Claim 24, wherein after placing the target in a lysis buffer, there is a step of adding phenol and chloroform into the lysis buffer with the target.

Claim 27. (Previously Presented) A method according to Claim 26, wherein after the adding step, there is a step of separating short length fragments of DNA, wherein the DNA is less than 100 base pairs in length from the target.

Claim 28. (Previously Presented) A method according to Claim 18, wherein the amplifying step comprises:

choosing a primer corresponding to a gene of the patient;

adding the primer to the DNA sequences; and

performing polymerase chain reaction on the DNA sequences with primer.

Claim 29. (Previously Presented) A method according to Claim 18, wherein the detecting step further includes determining the DNA sequence.

Claim 30. (Previously Presented) A method according to Claim 29, further comprising comparing the determined DNA sequence with known DNA sequences for corresponding DNA regions of the target.

Claim 31. (Previously Presented) A method according to Claim 18, further comprising the step of establishing whether the DNA sequence is associated with a cancer.

Claim 32. (Previously Presented) A method according to Claim 18, further comprising the step of establishing whether the DNA sequence is associated with a condition hazardous to the health of the patient.

Claim 33. (Previously Presented) A method according to Claim 18, wherein the amplifying step comprises cycling the DNA sequences in a polymerase chain reaction machine, with each cycle comprising a heating step to a temperature no greater than 99°C, and a cooling step to a temperature of 55°C in 5 minutes.

Claim 34. (Previously Presented) A method according to Claim 33, wherein the separating step includes a step of cutting one to three 2-6 μm thick histologic sections from the specimen.

Claim 35. (Previously Presented) A method according to Claim 32, wherein the biological specimen is a human tissue specimen.

Claim 36. (Previously Presented) The method of claim 18, wherein thirty or less separate tests are performed on a single sample.

Claim 37. (Previously Presented) The method of claim 18, further comprising using the results of the genotyping in relational database.

Claim 38. (Previously Presented) The method of claim 37, wherein the database is used to identify a new type of cancer.

Claim 39. (Previously Presented) The method of claim 37, wherein the database is used to devise a treatment plan to treat a patient with diagnosed cancer.

Claim 40. (Previously Presented) The method of claim 39, wherein the cancer is selected from the group consisting of colorectal cancer, lung cancer, pancreas adenocarinoma, genitourinary cancer, skin cancer, hematologic malignancy, thyroid cancer, endocrine cancer, breast cancer, renal cell carcinoma, and von Hippel Lindau disease.

Claim 41. (Previously Presented) The method of claim 32, wherein the condition hazardous to the health of the patient is selected from the group consisting of inherited diseases, genetic polymorphisms, and infectious diseases.

Claim 42. (Previously Presented) The method of claim 18, comprising the further step of diagnosing an inherited disease in a patient.

Claim 43. (Previously Presented) The method of claim 18, comprising the further step of determining a genetic polymorphism associated with a genetic disease in a patient.

Claim 44. (Previously Presented) The method of claim 18, comprising the further step of diagnosing an infectious disease in a patient.

Claim 45. (Previously Presented) The method of claim 18, comprising the further step of devising a course of treatment for a patient suffering from an infectious disease.

Claim 46. (New) The method of claim 18, wherein the microscopic sized target is about 0.25 cm^2 to about 0.5 cm^2 in size.